WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising:

a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:1 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600 or 1700 residues, or the full length of SEQ ID NO:1,

a nucleic acid sequence having at least 55% sequence identity to SEQ ID NO:3 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200 or 1250 residues, or the full length of SEQ ID NO:3,

a nucleic acid sequence having at least 65% sequence identity to SEQ ID NO:5 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800 residues, or the full length of SEQ ID NO:5,

a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:7 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300 residues, or the full length of SEQ ID NO:7,

a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:9 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600 residues, or the full length of SEQ ID NO:9,

a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700 residues, or the full length of SEQ ID NO:11,

a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:13 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1350 residues, or the full length of SEQ ID NO:13,

a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:15 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600 residues, or the full length of SEQ ID NO:15,

a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:17 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1350 residues, or the full length of SEQ ID NO:17,

a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:19 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:19,

a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:21 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400 residues, or the full length of SEQ ID NO:21, or

a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:23 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:23,

wherein the nucleic acid encodes at least one polypeptide having a glucosidase activity, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

2. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises:

a nucleic acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:1 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600 or 1700 residues, or the full length of SEQ ID NO:1;

a nucleic acid sequence having at least 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:3 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200 or 1250 residues, or the full length of SEQ ID NO:3;

a nucleic acid sequence having at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:5 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800 residues, or the full length of SEQ ID NO:5;

a nucleic acid sequence having at least 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:7 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300 residues, or the full length of SEQ ID NO:7;

a nucleic acid sequence having at least 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:9 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600 residues, or the full length of SEQ ID NO:9;

a nucleic acid sequence having at least 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:11 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700 residues, or the full length of SEQ ID NO:11;

a nucleic acid sequence having at least 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:13 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1350 residues, or the full length of SEQ ID NO:13;

a nucleic acid sequence having at least 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%

sequence identity to SEQ ID NO:15 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600 residues, or the full length of SEQ ID NO:15;

a nucleic acid sequence having at least 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:17 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1350 residues, or the full length of SEQ ID NO:17;

a nucleic acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:19 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:19;

a nucleic acid sequence having at least 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:21 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400 residues, or the full length of SEQ ID NO:21;

a nucleic acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:23 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:23.

3. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid comprises a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21 or SEQ ID NO:23.

4. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence encodes a polypeptide comprising a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12,

SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24.

5. The isolated or recombinant nucleic acid of claim 1, wherein the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

6. The isolated or recombinant nucleic acid of claim 1, wherein the glucosidase activity comprises an a-glucosidase activity.

7. The isolated or recombinant nucleic acid of claim 1, wherein the glucosidase activity comprises catalyzing the hydrolysis of an alpha-(1,4) glucose linkage, an alpha-(1,6) glucose linkage, an alpha-(1,2) glucose linkage, an alpha-(1,3) glucose linkage or a combination thereof.

8. The isolated or recombinant nucleic acid of claim 7, wherein the glucosidase activity comprises catalyzing the hydrolysis of alpha-(1,4) glucose linkages and alpha-(1,6) glucose linkages.

9. The isolated or recombinant nucleic acid of claim 1, wherein the glucosidase activity comprises hydrolyzing glucosidic bonds in a starch to produce maltodextrins.

10. The isolated or recombinant nucleic acid of claim 1, wherein the glucosidase activity comprises catalyzing the hydrolysis of both malto-oligosaccharides and liquefied starch.

11. The isolated or recombinant nucleic acid of claim 6, wherein the a-glucosidase activity comprises a 1,4-a-D-glucan hydrolase activity or a 1,6-a-D-glucan hydrolase activity.

12. The isolated or recombinant nucleic acid of claim 1, wherein the glucosidase activity comprises an exoglucosidase activity.

13. The isolated or recombinant nucleic acid of claim 6, wherein the a-glucosidase activity comprises hydrolyzing glucosidic bonds in a starch.

14. The isolated or recombinant nucleic acid of claim 1, wherein the glucosidase activity comprises catalyzing the hydrolysis of starch to alpha-D-glucose residues.

15. The isolated or recombinant nucleic acid of claim 1, wherein the glucosidase activity comprises cleaving a glucose residue from a reducing or a non-reducing end of a starch.

16. The isolated or recombinant nucleic acid of claim 1, wherein the glucosidase activity is thermostable.

17. The isolated or recombinant nucleic acid of claim 16, wherein the polypeptide retains a glucosidase activity under conditions comprising a temperature range of between about 37°C to about 95°C.

18. The isolated or recombinant nucleic acid of claim 17, wherein the polypeptide retains a glucosidase activity under conditions comprising a temperature range of between about 55°C to about 85°C, between about 70°C to about 95°C or between about 90°C to about 95°C.

19. The isolated or recombinant nucleic acid of claim 1, wherein the glucosidase activity is thermotolerant.

20. The isolated or recombinant nucleic acid of claim 19, wherein the polypeptide retains a glucosidase activity after exposure to a temperature in the range from between about 37°C to about 95°C.

21. The isolated or recombinant nucleic acid of claim 20, wherein the polypeptide retains a glucosidase activity after exposure to a temperature in the range from between about 55°C to about 85°C or between about 90°C to about 95°C.

22. An isolated or recombinant nucleic acid, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a nucleic acid comprising: a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21 or SEQ ID NO:23 or subsequences thereof, wherein the nucleic acid encodes a polypeptide having a glucosidase activity.

23. The isolated or recombinant nucleic acid of claim 23, wherein the nucleic acid is at least about 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript.

24. The isolated or recombinant nucleic acid of claim 22, wherein the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

25. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide with a glucosidase activity, wherein the probe comprises at least 10 consecutive bases of a sequence comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21 or SEQ ID NO:23, wherein the probe identifies the nucleic acid by binding or hybridization.

26. The nucleic acid probe of claim 25, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

27. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a glucosidase activity, wherein the probe comprises a nucleic acid comprising at least about 10 consecutive residues of a sequence comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21 or SEQ ID NO:23, or a sequence as set forth in claim 1 or claim 22.

28. The nucleic acid probe of claim 27, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

29. An amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide having an glucosidase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence as set forth in claim 1 or claim 22, or a subsequence thereof.

30. The amplification primer pair of claim 29, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence.

31. A method of amplifying a nucleic acid encoding a polypeptide having an glucosidase activity comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence as set forth in claim 1 or claim 22, or a subsequence thereof.

32. An expression cassette comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 22.

33. A vector comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 22.

34. A cloning vehicle comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 22, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

35. The cloning vehicle of claim 34, wherein the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector.

36. The cloning vehicle of claim 34, comprising a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

37. A transformed cell comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 22.

38. A transformed cell comprising an expression cassette as set forth in claim 32.

39. The transformed cell of claim 37 or claim 38, wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

40. A transgenic non-human animal comprising a sequence as set forth in claim 1 or claim 22.

41. The transgenic non-human animal of claim 40, wherein the animal is a mouse.

42. A transgenic plant comprising a sequence as set forth in claim 1 or claim 22.

43. The transgenic plant of claim 42, wherein the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

44. A transgenic seed comprising a sequence as set forth in claim 1 or claim 22.

45. The transgenic seed of claim 44, wherein the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

46. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 22, or a subsequence thereof.

47. The antisense oligonucleotide of claim 46, wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

48. A method of inhibiting the translation of an glucosidase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 22.

49. A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of a sequence as set forth in claim 1 or claim 22.

50. The double-stranded inhibitory RNA (RNAi) molecule of claim 49, wherein the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 or more duplex nucleotides in length.

51. A method of inhibiting the expression of an glucosidase in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of a sequence as set forth in claim 1 or claim 22.

52. An isolated or recombinant polypeptide comprising:

(a) a sequence having at least 80% sequence identity to SEQ ID NO:2 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550 residues, or the full length of SEQ ID NO:2,

a sequence having at least 55% sequence identity to SEQ ID NO:4 over a region of at least about 100, 150, 200, 250, 300, 350, 400 residues, or the full length of SEQ ID NO:4,

a sequence having at least 65% sequence identity to SEQ ID NO:6 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600 residues, or the full length of SEQ ID NO:6,

a sequence having at least 95% sequence identity to SEQ ID NO:8 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750 residues, or the full length of SEQ ID NO:8,

a sequence having at least 60% sequence identity to SEQ ID NO:10 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500 residues, or the full length of SEQ ID NO:10,

a sequence having at least 50% sequence identity to SEQ ID NO:12 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550 residues, or the full length of SEQ ID NO:12,

a sequence having at least 50% sequence identity to SEQ ID NO:14 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450 residues, or the full length of SEQ ID NO:14,

a sequence having at least 60% sequence identity to SEQ ID NO:16 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500 residues, or the full length of SEQ ID NO:16,

a sequence having at least 50% sequence identity to SEQ ID NO:18 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1350 residues, or the full length of SEQ ID NO:18,

a sequence having at least 80% sequence identity to SEQ ID NO:20 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:20,

a sequence having at least 95% sequence identity to SEQ ID NO:22 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400 residues, or the full length of SEQ ID NO:22, or

a sequence having at least 80% sequence identity to SEQ ID NO:24 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1650 residues, or the full length of SEQ ID NO:24,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or

(b) a polypeptide encoded by a nucleic acid comprising a sequence (i) having at least 80% sequence identity to SEQ ID NO:1, a nucleic acid sequence having at least 55% sequence identity to SEQ ID NO:3, a nucleic acid sequence having at least 65% sequence identity to SEQ ID NO:5, a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:7, a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:9, a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11, a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:13, a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:15, a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:17, a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:19, a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:21, or a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:23, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or, (ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, or subsequences thereof.

53. The isolated or recombinant polypeptide of claim 52, wherein the polypeptide comprises

a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:2 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550 residues, or the full length of SEQ ID NO:2;

a sequence having at least 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:4 over a region of at least about 100, 150, 200, 250, 300, 350, 400 residues, or the full length of SEQ ID NO:4;

a sequence having at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:6 over a

region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600 residues, or the full length of SEQ ID NO:6;

a sequence having at least 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:8 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750 residues, or the full length of SEQ ID NO:8;

a sequence having at least 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:10 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500 residues, or the full length of SEQ ID NO:10;

a sequence having at least 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:12 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550 residues, or the full length of SEQ ID NO:12;

a sequence having at least 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:14 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450 residues, or the full length of SEQ ID NO:14;

a sequence having at least 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:16 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500 residues, or the full length of SEQ ID NO:16;

a sequence having at least 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:18 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450 residues, or the full length of SEQ ID NO:18;

a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:20 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550 residues, or the full length of SEQ ID NO:20;

a sequence having at least 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:22 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450 residues, or the full length of SEQ ID NO:22;

a sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:24 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550 residues, or the full length of SEQ ID NO:24.

54. The isolated or recombinant polypeptide of claim 96, wherein the polypeptide comprises an amino acid sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24.

55. The isolated or recombinant polypeptide of claim 52, wherein the polypeptide has a glucosidase activity.

56. The isolated or recombinant polypeptide of claim 52, wherein the glucosidase activity comprises an a-glucosidase activity.

57. The isolated or recombinant polypeptide of claim 52, wherein the glucosidase activity comprises catalyzing the hydrolysis of an alpha-(1,4) glucose linkage, an alpha-(1,6) glucose linkage, an alpha-(1,2) glucose linkage, an alpha-(1,3) glucose linkage or a combination thereof.

58. The isolated or recombinant polypeptide of claim 57, wherein the glucosidase activity comprises catalyzing the hydrolysis of alpha-(1,4) glucose linkages and alpha-(1,6) glucose linkages.

59. The isolated or recombinant nucleic polypeptide of claim 52, wherein the glucosidase activity comprises hydrolyzing glucosidic bonds in a starch to produce maltodextrins.

60. The isolated or recombinant polypeptide of claim 52, wherein the glucosidase activity comprises catalyzing the hydrolysis of both malto-oligosaccharides and liquefied starch.

61. The isolated or recombinant polypeptide of claim 55, wherein the a-glucosidase activity comprises a 1,4-a-D-glucan hydrolase activity or a 1,6-a-D-glucan hydrolase activity.

62. The isolated or recombinant polypeptide of claim 52, wherein the glucosidase activity comprises an exoglucosidase activity.

63. The isolated or recombinant polypeptide of claim 52, wherein the glucosidase activity comprises hydrolyzing glucosidic bonds in a starch.

64. The isolated or recombinant polypeptide of claim 52, wherein the glucosidase activity comprises catalyzing the hydrolysis of starch to alpha-D-glucose residues.

65. The isolated or recombinant polypeptide of claim 52, wherein the glucosidase activity comprises cleaving a glucose residue from a reducing or a non-reducing end of a starch.

66. The isolated or recombinant polypeptide of claim 55, wherein the glucosidase activity is thermostable.

67. The isolated or recombinant polypeptide of claim 66, wherein the polypeptide retains a glucosidase activity under conditions comprising a temperature range of between about 37°C to about 95°C.

68. The isolated or recombinant polypeptide of claim 66, wherein the polypeptide retains a glucosidase activity under conditions comprising a temperature range of between about 55°C to about 85°C, between about 70°C to about 95°C or between about 90°C to about 95°C.

69. The isolated or recombinant polypeptide of claim 55, wherein the glucosidase activity is thermotolerant.

70. The isolated or recombinant polypeptide of claim 69, wherein the polypeptide retains a glucosidase activity after exposure to a temperature in the range from between about 37°C to about 95°C.

71. The isolated or recombinant polypeptide of claim 69, wherein the polypeptide retains a glucosidase activity after exposure to a temperature in the range from between about 55°C to about 85°C or between about 90°C to about 95°C.

72. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 52 and lacking a signal sequence.

73. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 52 and having a heterologous signal sequence.

74. The isolated or recombinant polypeptide of claim 55, wherein the glucosidase activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein.

75. The isolated or recombinant polypeptide of claim 70, wherein the thermotolerance comprises retention of at least half of the specific activity of the glucosidase at 37°C after being heated to an elevated temperature.

76. The isolated or recombinant polypeptide of claim 70, wherein the thermotolerance comprises retention of specific activity at 37°C in the range from about

500 to about 1200 units per milligram of protein after being heated to an elevated temperature.

77. The isolated or recombinant polypeptide of claim 52, wherein the polypeptide comprises at least one glycosylation site.

78. The isolated or recombinant polypeptide of claim 77, wherein the glycosylation is an N-linked glycosylation.

79. The isolated or recombinant polypeptide of claim 78, wherein the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

80. The isolated or recombinant polypeptide of claim 55, wherein the polypeptide retains a glucosidase activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0.

81. The isolated or recombinant polypeptide of claim 55, wherein the polypeptide retains a glucosidase activity under conditions comprising about pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.

82. A protein preparation comprising a polypeptide as set forth in claim 52, wherein the protein preparation comprises a liquid, a solid or a gel.

83. A heterodimer comprising a polypeptide as set forth in claim 52 and a second domain.

84. The heterodimer of claim 83, wherein the second domain is a polypeptide and the heterodimer is a fusion protein.

85. The heterodimer of claim 84, wherein the second domain is an epitope or a tag.

86. A homodimer comprising a polypeptide as set forth in claim 52.

87. An immobilized polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 52, or a subsequence thereof.

88. The immobilized polypeptide of claim 87, wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

89. An array comprising an immobilized polypeptide as set forth in claim 52.

90. An array comprising an immobilized nucleic acid as set forth in claim 1 or claim 22.

91. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 52.

92. The isolated or recombinant antibody of claim 91, wherein the antibody is a monoclonal or a polyclonal antibody.

93. A hybridoma comprising an antibody that specifically binds to a polypeptide as set forth in claim 52.

94. A food supplement for an animal comprising a polypeptide as set forth in claim 52, or a subsequence thereof.

95. The food supplement of claim 94, wherein the polypeptide is glycosylated.

96. An edible enzyme delivery matrix comprising a polypeptide as set forth in claim 52.

97. The edible enzyme delivery matrix of claim 96, wherein the delivery matrix comprises a pellet.

98. The edible enzyme delivery matrix of claim 96, wherein the polypeptide is glycosylated.

99. The edible enzyme delivery matrix of claim 96, wherein the polypeptide has a thermotolerant or a thermostable glucosidase activity.

100. A method of isolating or identifying a polypeptide with a glucosidase activity comprising the steps of:

(a) providing an antibody as set forth in claim 91;

(b) providing a sample comprising polypeptides; and

(c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having a glucosidase activity.

101. A method of making an anti-glucosidase antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 or claim 22 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-glucosidase antibody.

102. A method of making an anti-glucosidase antibody comprising administering to a non-human animal a polypeptide as set forth in claim 52 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-glucosidase antibody.

103. A method of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises a sequence as set forth in claim 1 or claim 22; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

104. The method of claim 103, further comprising transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

105. A method for identifying a polypeptide having a glucosidase activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 55;

(b) providing a glucosidase substrate; and

(c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a glucosidase activity.

106. The method of claim 105 wherein the substrate is a starch.

107. A method for identifying a glucosidase substrate comprising the following steps:

(a) providing a polypeptide as set forth in claim 55;

(b) providing a test substrate; and

(c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a glucosidase substrate.

108. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has a sequence as set forth in claim 1 or claim 22;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

109. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) providing a polypeptide having a sequence as set forth in claim 52;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

110. A method for identifying a modulator of a glucosidase activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 55;

(b) providing a test compound;

(c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the glucosidase, wherein a change in the glucosidase activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the glucosidase activity.

111. The method of claim 110, wherein the glucosidase activity is measured by providing a glucosidase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product.

112. The method of claim 111, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of glucosidase activity.

113. The method of claim 111, wherein an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of glucosidase activity.

114. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence as set forth in claim 52, a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22 ,

115. The computer system of claim 114, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

116. The computer system of claim 115, wherein the sequence comparison algorithm comprises a computer program that indicates polymorphisms.

117. The computer system of claim 114, further comprising an identifier that identifies one or more features in said sequence.

118. A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 52; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

119. A method for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 52; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22; and (b) identifying one or more features in the sequence with the computer program.

120. A method for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 52 or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22; and (b) determining differences between the first sequence and the second sequence with the computer program.

121. The method of claim 120, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

122. The method of claim 120, further comprising an identifier that identifies one or more features in a sequence.

123. The method of claim 122, comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

124. A method for isolating or recovering a nucleic acid encoding a polypeptide with a glucosidase activity from an environmental sample comprising the steps of:

(a) providing an amplification primer sequence pair as set forth in claim 29;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide with a glucosidase activity from an environmental sample.

125. The method of claim 124, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, or a subsequence thereof.

126. A method for isolating or recovering a nucleic acid encoding a polypeptide with a glucosidase activity from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising a sequence as set forth in claim 1 or claim 22, or a subsequence thereof;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a glucosidase activity from an environmental sample.

127. The method of claim 124 or claim 126, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample.

128. The method of claim 127, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

129. A method of generating a variant of a nucleic acid encoding a polypeptide with a glucosidase activity comprising the steps of:

(a) providing a template nucleic acid comprising a sequence as set forth in claim 1 or claim 22; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid.

130. The method of claim 129, further comprising expressing the variant nucleic acid to generate a variant glucosidase polypeptide.

131. The method of claim 129, wherein the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

132. The method of claim 129, wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

133. The method of claim 129, wherein the method is iteratively repeated until a glucosidase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced.

134. The method of claim 133, wherein the variant glucosidase polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature.

135. The method of claim 133, wherein the variant glucosidase polypeptide has increased glycosylation as compared to the glucosidase encoded by a template nucleic acid.

136. The method of claim 133, wherein the variant glucosidase polypeptide has a glucosidase activity under a high temperature, wherein the glucosidase encoded by the template nucleic acid is not active under the high temperature.

137. The method of claim 129, wherein the method is iteratively repeated until a glucosidase coding sequence having an altered codon usage from that of the template nucleic acid is produced.

138. The method of claim 129, wherein the method is iteratively repeated until a glucosidase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

139. A method for modifying codons in a nucleic acid encoding a polypeptide with a glucosidase activity to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a glucosidase activity comprising a sequence as set forth in claim 1 or claim 22; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

140. A method for modifying codons in a nucleic acid encoding a glucosidase polypeptide, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a glucosidase activity comprising a sequence as set forth in claim 1 or claim 22; and,

(b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a glucosidase.

141. A method for modifying codons in a nucleic acid encoding a glucosidase polypeptide to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a glucosidase polypeptide comprising a sequence as set forth in claim 1 or claim 22; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

142. A method for modifying a codon in a nucleic acid encoding a polypeptide having a glucosidase activity to decrease its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a glucosidase polypeptide comprising a sequence as set forth in claim 1 or claim 22; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell.

143. The method of claim 141 or 142, wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

144. A method for producing a library of nucleic acids encoding a plurality of modified glucosidase active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, or a subsequence thereof, and the nucleic acid encodes a glucosidase active site or a glucosidase substrate binding site;

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing

a library of nucleic acids encoding a plurality of modified glucosidase active sites or substrate binding sites.

145. The method of claim 144, comprising mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, gene site-saturation mutagenesis (GSSM™), or a synthetic ligation reassembly (SLR).

146. The method of claim 144, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

147. The method of claim 144, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

148. A method for making a small molecule comprising the following steps:

(a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises a glucosidase enzyme encoded by a nucleic acid comprising a sequence as set forth in claim 1 or claim 22;

(b) providing a substrate for at least one of the enzymes of step (a); and

(c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

149. A method for modifying a small molecule comprising the following steps:

(a) providing a glucosidase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence as set forth in claim 1 or claim 22;

(b) providing a small molecule; and

(c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the glucosidase enzyme, thereby modifying a small molecule by a glucosidase enzymatic reaction.

150. The method of claim 149, comprising a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the glucosidase enzyme.

151. The method of claim 149, further comprising a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions.

152. The method of claim 151, further comprising the step of testing the library to determine if a particular modified small molecule which exhibits a desired activity is present within the library.

153. The method of claim 152, wherein the step of testing the library further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

154. A method for determining a functional fragment of a glucosidase enzyme comprising the steps of:

(a) providing a glucosidase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22; and

(b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a glucosidase activity, thereby determining a functional fragment of a glucosidase enzyme.

155. The method of claim 154, wherein the glucosidase activity is measured by providing a glucosidase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

156. A method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps:

(a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid comprising a sequence as set forth in claim 1 or claim 22;

(b) culturing the modified cell to generate a plurality of modified cells;

(c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and,

(d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis.

157. The method of claim 155, wherein the genetic composition of the cell is modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene.

158. The method of claim 157, further comprising selecting a cell comprising a newly engineered phenotype.

159. The method of claim 158, further comprising culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

160. A method for hydrolyzing a starch comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing a composition comprising a starch; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the polypeptide hydrolyzes the starch.

161. The method as set forth in claim 160, wherein the composition comprises an a-1,4-glucosidic bond or an a-1,6-glucosidic bond.

162. A method for liquefying or removing a starch from a composition comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing a composition comprising a starch; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the polypeptide removes or liquefies the starch.

163. A method of increasing thermotolerance or thermostability of a glucosidase polypeptide, the method comprising glycosylating a glucosidase polypeptide, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22, thereby increasing the thermotolerance or thermostability of the glucosidase polypeptide.

164. The method of claim 163, wherein the glucosidase specific activity is thermostable or thermotolerant at a temperature in the range from greater than about 37°C to about 95°C.

165. A method for overexpressing a recombinant glucosidase polypeptide in a cell comprising expressing a vector comprising a nucleic acid sequence having a sequence as set forth in claim 1 or claim 22, wherein overexpression is effected

by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

166. A detergent composition comprising a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22, wherein the polypeptide comprises a glucosidase activity.

167. The detergent composition of claim 166, wherein the glucosidase is a nonsurface-active glucosidase or a surface-active glucosidase.

168. The detergent composition of claim 166, wherein the glucosidase is formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel form, a paste or a slurry form.

169. A method for washing an object comprising the following steps:

(a) providing a composition comprising a polypeptide having a glucosidase activity, wherein the polypeptide comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing an object; and

(c) contacting the polypeptide of step (a) and the object of step (b) under conditions wherein the composition can wash the object.

170. A method for hydrolyzing a starch in a feed or a food prior to consumption by an animal comprising the following steps:

(a) obtaining a feed material comprising a starch, wherein the starch can be hydrolyzed by a polypeptide having a glucosidase activity, wherein the polypeptide comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22; and

(b) adding the polypeptide of step (a) to the feed or food material in an amount sufficient for a sufficient time period to cause hydrolysis of the starch and formation of a treated food or feed, thereby hydrolyzing the starch in the food or the feed prior to consumption by the animal.

171. The method as set forth in claim 170, wherein the food or feed comprises rice, corn, barley, wheat, legumes, or potato.

172. A feed or a food comprising a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

173. A composition comprising a starch and a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

174. A textile comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

175. A method for textile desizing comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing a fabric; and

(c) contacting the polypeptide of step (a) and the fabric of step (b) under conditions wherein the glucosidase can desize the fabric.

176. A paper or paper product or paper pulp comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

177. A method for deinking of paper or fibers comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing a composition comprising paper or fiber; and

(c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the polypeptide can deink the paper or fiber.

178. A method for treatment of lignocellulosic fibers comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing a lignocellulosic fiber; and

(c) contacting the polypeptide of step (a) and the fiber of step (b) under conditions wherein the polypeptide can treat the fiber thereby improving the fiber properties.

179. A high-maltose or a high-glucose liquid or syrup comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

180. A method for producing a high-maltose or a high-glucose syrup comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing a composition comprising a starch; and

(c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the polypeptide of step (a) can hydrolyze the composition of step (b), thereby producing a high-maltose or a high-glucose syrup.

181. The method as set forth in claim 180, wherein the starch is from rice, corn, barley, wheat, legumes, potato, or sweet potato.

182. A method for improving the flow of the starch-containing production fluids comprising the following steps:

(a) providing a polypeptide having a glucosidase activity, wherein the polypeptide comprises a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing production fluid comprising a starch; and

(c) contacting the polypeptide of step (a) and the production fluid of step (b) under conditions wherein the glucosidase can hydrolyze the starch in the production fluid, thereby improving its flow by decreasing its density.

183. The method as set forth in claim 182, wherein the production fluid is from a subterranean formation.

184. An anti-staling composition comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

185. A method for preventing staling of a baked product comprising the following steps:

(a) providing a polypeptide comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing a composition used for baking comprising a starch;

(c) combining the polypeptide of step (a) with the composition of the step (b) under conditions wherein the polypeptide can hydrolyze the starch in the composition used for baking, thereby preventing staling of the baked product.

186. The method as set forth in claim 185, wherein the baked product is a bread or a bread product.

187. A method for using glucosidase in brewing or alcohol production comprising the following steps:

(a) providing a polypeptide comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22;

(b) providing a composition used for brewing or in alcohol production comprising a starch or a polysaccharide;

(c) combining the polypeptide of step (a) with the composition of the step (b) under conditions wherein the polypeptide can hydrolyze the starch or the polysaccharide in the composition used for brewing or alcohol production.

188. The method as set forth in claim 187, wherein the composition comprising the starch or the polysaccharide is a beer.

189. An alcoholic beverage comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

190. A beer comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

191. A pharmaceutical composition comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

192. The expression cassette of claim 32, wherein the nucleic acid is operably linked to a plant promoter.

193. The expression cassette of claim 192, further comprising a plant expression vector.

194. The expression cassette of claim 193, wherein the plant expression vector comprises a plant virus.

195. The expression cassette of claim 192, wherein the plant promoter comprises a potato promoter, a rice promoter, a corn promoter, a wheat or a barley promoter.

196. The expression cassette of claim 192, wherein the promoter comprises a promoter derived from T-DNA of *Agrobacterium tumefaciens*.

197. The expression cassette of claim 192, wherein the promoter is a constitutive promoter.

198. The expression cassette of claim 197, wherein the constitutive promoter is CaMV35S.

199. The expression cassette of claim 192, wherein the promoter is an inducible promoter or a tissue-specific promoter.

200. The expression cassette of claim 199, wherein the tissue-specific promoter is a seed-specific, a leaf-specific, a root-specific, a stem-specific or an abscission-induced promoter.

201. The transformed cell of claim 39, wherein the plant cell is a potato, rice, corn, wheat, tobacco or barley cell.

202. A method of making a transgenic plant comprising the following steps:

(a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 22, thereby producing a transformed plant cell;

(b) producing a transgenic plant from the transformed cell.

203. The method as set forth in claim 202, wherein the step (a) further comprises introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts.

204. The method as set forth in claim 202, wherein the step (a) comprises introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment.

205. The method as set forth in claim 202, wherein the step (a) comprises introducing the heterologous nucleic acid sequence into the plant cell DNA using an *Agrobacterium tumefaciens* host.

206. A method of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps:

(a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 22;

(b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

207. An isolated or recombinant signal sequence consisting of a sequence as set forth in residues 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30 or 1 to 31, 1 to 32 or 1 to 33 of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24.

208. An isolated or recombinant signal sequence comprising a sequence as set forth in residues 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30 or 1 to 31, 1 to 32 or 1 to 33 of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22 or SEQ ID NO:24.

209. A chimeric protein comprising a first domain comprising a signal sequence as set forth in claim 207 and at least a second domain.

210. The chimeric protein of claim 209, wherein the protein is a fusion protein.

211. The chimeric protein of claim 209, wherein the second domain comprises an enzyme.

212. The chimeric protein of claim 211, wherein the enzyme is a glucosidase.

213. A chimeric polypeptide comprising at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 207, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

214. The chimeric polypeptide of claim 213, wherein the heterologous polypeptide or peptide is not a glucosidase.

215. The chimeric polypeptide of claim 213, wherein the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or a catalytic domain (CD).

216. An isolated or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 213 and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

217. An oral care product comprising a polypeptide as set forth in claim 55, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 22.

218. The oral care product of claim 217, wherein the product comprises a toothpaste, a dental cream, a gel or a tooth powder, an odontic, a mouth wash, a pre- or post brushing rinse formulation, a chewing gum, a lozenge or a candy.